AMENDMENTS TO THE CLAIMS

1. **(Currently amended)** A method for ~~immobilising~~ immobilizing a protein on a microporous material, said microporous material is selected from the group consisting of zeolite or a similar solid ~~surfaces~~ surface whereby loss of activity of said protein is less than 10% of the initial activity prior to ~~immobilising~~ immobilizing, ~~the method~~ comprising the steps of:

(i) selecting a polypeptide tag capable of binding to the surface,

(ii) ~~immobilise~~ immobilizing said protein by the steps of:

(a) attaching said polypeptide tag to the protein, and

(b) binding said polypeptide tag to the solid surface

wherein step (a) and (b) ~~is~~ are performed simultaneously or sequentially and when performed sequentially, the order of step (a) and (b) is random, ~~subject to the limitation that the~~ further wherein the polypeptide tag does not consist only of histidine residues.

2. **(Currently amended)** ~~A~~ The method according to claim 1 wherein the binding in step (i) is a specifically binding of the polypeptide tag to the surface.

3. **(Currently amended)** ~~A~~ The method according to claim 1 ~~or 2~~ wherein the polypeptide tag comprises at least two lysine residues.

4. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-3~~ claim 1 wherein the polypeptide tag comprises at the most 21-500 of amino acid residues.

5. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-4~~ claim 1 wherein said polypeptide tag has at least 30-100% amino acid sequence identity to SEQ ID NO 1.

6. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-4~~ claim 1 wherein said polypeptide tag has at least 30-100% amino acid sequence identity to SEQ ID NO 2.

7. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-6~~ claim 1 wherein the binding in step (i) is enhanced by repeating said polypeptide tag at least 2, 3, 4, 7, 10, 50, or 100 times.

8. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-7~~ claim 1 wherein the avidity of the polypeptide tag for the surface is enhanced by repeating said polypeptide tag at least 2, 3, 4, 7, 10, 50, 100 times.

9. **(Currently amended)** ~~A~~ The method according to claim 7 ~~or 8~~ wherein the amino acid sequence identity between the repeating polypeptide sequences is at least 30-100%.

10. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-9~~ claim 1 wherein the protein is ~~a protein~~ expressed on the surface of a cell.

11. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-10~~ claim 1 wherein said attachment of the polypeptide tag to the protein provides a fusion protein.

12. **(Currently amended)** ~~A~~ The method according to claim 11 wherein said fusion protein is recombinantly provided.

13. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-12~~ claim 1 wherein the polypeptide tag is attached to the protein by chemical treatment.

14. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-13~~ claim 1 wherein the surface comprises at least one aluminum moiety, at least one silicate moiety and/or at least one phosphate moiety.

15. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-14~~ claim 1 wherein the similar solid surface is selected from the group consisting of meso- and microporous materials including hydrotalcite, clay, aluminosilicate, oxide powders, activated carbon, mica, glass, clinoptolite, gismondine zeolite, alluminate and quartz.

16. **(Currently amended)** ~~A~~ The method according to claim 15 wherein the zeolite is either naturally occurring or synthetically produced.

17. **(Currently amended)** ~~A~~ The method according to ~~any of claims~~ claim 15 ~~or 16~~ wherein the meso- and microporous material is selected from the group of zeolites consisting of AFI, EMT, FAU and MFI.

18. **(Currently amended)** ~~A~~ The method according to ~~any of claims 15-17~~ claim 15 wherein the zeolite has a pore size in the range selected from the group consisting of 1-50 Å, ~~such as~~ 1-40 Å, ~~e.g.~~ 1-30 Å, ~~such as~~ 1-20 Å, ~~e.g.~~ 1-15 Å, ~~such as~~ 2-10 Å, e.g. 3-8 Å, ~~such as~~ 5-8 Å, ~~e.g.~~ and 6-8 Å.

19. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-18~~ claim 1 wherein the protein is selected from the group consisting of an antibody, an antigen, a receptor, a biotin, an avidin, a hormone, a lectin, a sugar, an enzyme and a protease.

20. **(Currently amended)** ~~A~~ The method according to ~~any of claims 1-19~~ claim 1 wherein the polypeptide tag is bound directly to the solid surface.

21. **(Currently amended)** A polypeptide tag that is capable of controlling the orientation of proteins ~~immobilised~~ immobilized on a microporous material, wherein said microporous material is selected from the group consisting of zeolite ~~or~~ and similar solid surfaces.

22. **(Currently amended)** ~~A~~ The polypeptide tag according to claim 21 wherein the polypeptide tag comprises at least two lysine residues.

23. **(Currently amended)** ~~A~~ The polypeptide tag according to claim 21 ~~or 22~~ wherein the polypeptide tag comprises at the most 21-500 amino acid residues.

24. **(Currently amended)** ~~A~~ The polypeptide tag according to ~~any of claims 21-23~~ claim 21 wherein the polypeptide tag is provided on at least one subunit of a protein.

25. **(Currently amended)** ~~A~~ The polypeptide tag according to ~~any of claims 21-24~~ claim 21 wherein said polypeptide tag has at least 30-100% amino acid sequence identity to SEQ ID NO 1.

26. **(Currently amended)** ~~A~~ The polypeptide tag according to ~~any of claims 21-24~~ claim 21 wherein said polypeptide tag has at least 30-100% amino acid sequence identity to SEQ ID NO 2.

27. **(Currently amended)** A method for isolating an analyte from a liquid sample, said method ~~comprises~~ comprising ~~the steps of~~:

(i) selecting a protein ~~immobilised~~ immobilized according to the method of ~~any of claims 1-20,~~ claim 1, wherein said protein is capable of specifically binding to the analyte,

(ii) contacting said ~~immobilised~~ immobilized protein with the liquid sample,

(iii) permitting said ~~immobilised~~ immobilized protein to react with the analyte to obtain a complex of the ~~immobilised~~ immobilized protein and the analyte,

(iv) optionally washing said complex, and

(v) eluting the analyte from said complex.

28. **(Currently amended)** ~~A~~ The method according to claim 27 wherein the liquid sample is selected from the group consisting of ~~a~~ fermentation medium, wastewater, blood, milk, ~~and~~ urine, ~~diary~~ dairy products and ~~/or~~ a chemical reaction.

29. **(Currently amended)** ~~A~~ The method according to ~~any of claims 27-28~~ claim 27 wherein the ~~immobilised~~ immobilized protein is reused.

30. **(Currently amended)** ~~Use of a protein immobilised according to the method of any of claims 1-20 as~~ A method of purifying analyte comprising contacting said analyte with a column chromatography ~~column~~ material comprising a protein immobilized using ~~for the purification of an analyte~~ method of claim 1.

31. **(Currently amended)** ~~Use~~ A method of hydrolyzing a molecule comprising contacting said molecule with a protein ~~immobilised~~ immobilized using ~~according to~~ the method of ~~any of claims 1-20 for the hydrolysis of a molecule~~ claim 1.

32. **(Currently amended)** ~~A~~ The cell comprising a surface molecule comprising the polypeptide tag according to ~~any of claims 21-26~~ claim 21.

33. **(Currently amended)** A material having at least one surface onto which a polypeptide tag has been bound, wherein said polypeptide tag has at least 30-100% identity to SEQ ID NO. 1 or SEQ ID NO. 2.

34. **(Currently amended)** ~~A~~ The material according to claim 33 wherein the surface is selected from the group consisting of meso- and microporous materials including zeolite, hydrotalcite, clay, aluminosilicate, oxide powders, activated carbon, mica, glass, clinoptolite, gismondine zeolite, alluminate and quartz.

35. **(Currently amended)** A fusion protein ~~having~~ bound to a polypeptide tag ~~bound~~, wherein said polypeptide tag has at least 30-100% identity to SEQ ID NO. 1 or SEQ ID NO. 2.